

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/084,491A

1652

#8

DATE: 05/28/1999
TIME: 11:35:52

INPUT SET: S32049.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

ENTERED

(1) General Information:

(i) APPLICANT: MOORE, PAUL A.
RUBEN, STEVEN M.
EBNER, REINHARD

(ii) TITLE OF INVENTION: TISSUE PLASMINOGEN ACTIVATOR-LIKE PROTEASE

(iii) NUMBER OF SEQUENCES: 16

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
(B) STREET: 9410 KEY WEST AVENUE
(C) CITY: ROCKVILLE
(D) STATE: MD
(E) COUNTRY: USA
(F) ZIP: 20850

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/084,491
(B) FILING DATE: 27-MAY-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: BROOKES, ANDERS A.
(B) REGISTRATION NUMBER: 36,373
(C) REFERENCE/DOCKET NUMBER: PF378

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (301) 309-8504
(B) TELEFAX: (301) 309-8439

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2329 base pairs
(B) TYPE: nucleic acid

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47      (C) STRANDEDNESS: single
48      (D) TOPOLOGY: linear
49
50      (ii) MOLECULE TYPE: DNA (genomic)
51
52
53      (ix) FEATURE:
54          (A) NAME/KEY: CDS
55          (B) LOCATION: 124..913
56
57      (ix) FEATURE:
58          (A) NAME/KEY: sig_peptide
59          (B) LOCATION: 124..184
60
61      (ix) FEATURE:
62          (A) NAME/KEY: mat_peptide
63          (B) LOCATION: 187..913
64
65
66
67      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
68
69      TTACCAGAAC AGCATAACAA GGGCAGGTCT GACTGCAAGC TGGGACTGGG AGGCAGAGCC      60
70
71      GCCGCCAAGG GGGCCTCGGT TAAACACTGG TCGTTCAATC ACCTGCAAGA CGAAGAGGCA      120
72
73      AGG ATG CTG TTG GCC TGG GTA CAA GCA TTC CTC GTC AGC AAC ATG CTC      168
74      Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu
75      -21 -20 -15 -10
76
77      CTA GCA GAA GCC TAT GGA TCT GGA GGC TGT TTC TGG GAC AAC GGC CAC      216
78      Leu Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His
79      -5 1 5 10
80
81      CTG TAC CGG GAG GAC CAG ACC TCC CCC GCG CCG GGC CTC CGC TGC CTC      264
82      Leu Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu
83      15 20 25
84
85      AAC TGG CTG GAC GCG CAG AGC GGG CTG GCC TCG GCC CCC GTG TCG GGG      312
86      Asn Trp Leu Asp Ala Gln Ser Gly Leu Ala Ser Ala Pro Val Ser Gly
87      30 35 40
88
89      GCC GGC AAT CAC AGT TAC TGC CGA AAC CCG GAC GAG GAC CCG CGC GGG      360
90      Ala Gly Asn His Ser Tyr Cys Arg Asn Pro Asp Glu Asp Pro Arg Gly
91      45 50 55
92
93      CCC TGG TGC TAC GTC AGT GGC GAG GCC GGC GTC CCT GAG AAA CGG CCT      408
94      Pro Trp Cys Tyr Val Ser Gly Glu Ala Gly Val Pro Glu Lys Arg Pro
95      60 65 70
96
97      TGC GAG GAC CTG CGC TGT CCA GAG ACC ACC TCC CAG GCC CTG CCA GCC      456
98      Cys Glu Asp Leu Arg Cys Pro Glu Thr Thr Ser Gln Ala Leu Pro Ala
99      75 80 85 90

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100																	
101	TTC	ACG	ACA	GAA	ATC	CAG	GAA	GCG	TCT	GAA	GGG	CCA	GGT	GCA	GAT	GAG	504
102	Phe	Thr	Thr	Glu	Ile	Gln	Glu	Ala	Ser	Glu	Gly	Pro	Gly	Ala	Asp	Glu	
103					95					100					105		
104																	
105	GTG	CAG	GTG	TTC	GCT	CCT	GCC	AAC	GCC	CTG	CCC	GCT	CGG	AGT	GAG	GCG	552
106	Val	Gln	Val	Phe	Ala	Pro	Ala	Asn	Ala	Leu	Pro	Ala	Arg	Ser	Glu	Ala	
107				110					115					120			
108																	
109	GCA	GCT	GTG	CAG	CCA	GTG	ATT	GGG	ATC	AGC	CAG	CGG	GTG	CGG	ATG	AAC	600
110	Ala	Ala	Val	Gln	Pro	Val	Ile	Gly	Ile	Ser	Gln	Arg	Val	Arg	Met	Asn	
111			125					130					135				
112																	
113	TCC	AAG	GAG	AAA	AAG	GAC	CTG	GGA	ACT	CTG	GGC	TAC	GTG	CTG	GGC	ATT	648
114	Ser	Lys	Glu	Lys	Lys	Asp	Leu	Gly	Thr	Leu	Gly	Tyr	Val	Leu	Gly	Ile	
115		140					145					150					
116																	
117	ACC	ATG	ATG	GTG	ATC	ATC	ATT	GCC	ATC	GGA	GCT	GGC	ATC	ATC	TTG	GGC	696
118	Thr	Met	Met	Val	Ile	Ile	Ile	Ala	Ile	Gly	Ala	Gly	Ile	Ile	Leu	Gly	
119	155					160					165					170	
120																	
121	TAC	TCC	TAC	AAG	AGG	GGG	AAG	GAT	TTG	AAA	GAA	CAG	CAT	GAT	CAG	AAA	744
122	Tyr	Ser	Tyr	Lys	Arg	Gly	Lys	Asp	Leu	Lys	Glu	Gln	His	Asp	Gln	Lys	
123					175					180					185		
124																	
125	GTA	TGT	GAG	AGG	GAG	ATG	CAG	CGA	ATC	ACT	CTG	CCC	TTG	TCT	GCC	TTC	792
126	Val	Cys	Glu	Arg	Glu	Met	Gln	Arg	Ile	Thr	Leu	Pro	Leu	Ser	Ala	Phe	
127				190					195					200			
128																	
129	ACC	AAC	CCC	ACC	TGT	GAG	ATT	GTG	GAT	GAG	AAG	ACT	GTC	GTG	GTC	CAC	840
130	Thr	Asn	Pro	Thr	Cys	Glu	Ile	Val	Asp	Glu	Lys	Thr	Val	Val	Val	His	
131			205					210					215				
132																	
133																	
134	ACC	AGC	CAG	ACT	CCA	GTT	GAC	CCT	CAG	GAG	GGC	AGC	ACC	CCC	CTT	ATG	888
135	Thr	Ser	Gln	Thr	Pro	Val	Asp	Pro	Gln	Glu	Gly	Ser	Thr	Pro	Leu	Met	
136		220					225					230					
137																	
138	GGC	CAG	GCC	GGG	ACT	CCT	GGG	GCC	T	GAGCCCCCCC AGTGGGCAGG							933
139	Gly	Gln	Ala	Gly	Thr	Pro	Gly										

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153
154 CTTGAGTGGC ATACACTGTT ATTCATGGTT AAGGTAAAGC AGGTCAAGGG ATGGCATTGA 1353
155
156 AAAAATATAT TTAGTTTTTA AAATATTTGG GATGGAACTC CCTACTGACC TCTGACAACT 1413
157
158 GGAAACGAGT TTGTACTGAA GTCAGAACTT TGGGTTGGGA ATGAGATCTA GGTTGTGGCT 1473
159
160 GCTGGTATGC TTCAGCTTGC TGGCAATGAT GTGCCTTGAC AACCGTGGGC CAGGCCTGGG 1533
161
162 CCCAGGGACT CTTCTGTTT CATAAGGAAA GGAAGAATTG CACTGAGCAT TCCACTTAGG 1593
163
164 AAGAGGATAG AGAAGGATCT GCTCCGCCTT TGGCCACAGG AGCAGAGGCA GACCTGGGAT 1653
165
166 GCCCCAGTTT CTCTTCAGGG ATGGATAGTG ACCTGTCTTC ATTTTGCACA GGTAAGAGAG 1713
167
168 TAGTTAGCTA ACCTATGGGA ATTATACTGT GGGGCCTTGT GAGCTGCTTC TAAGAGGCTA 1773
169
170 ACCTGGAAAC TAAGCTCAGA GGCAAGGTAA TAAAGCACTT CAGGGCTTGC TCCCCAAGTG 1833
171
172 GGCCTGATTT AGCAGGTGGT CTGCGGGCGT CCAGGTCAGC ACCTTCCTGT AGGGCACTGG 1893
173
174 GGCTAGGGTC ACAGCCCCTA ACTCATAAAG CAATCAAAGA ACCATTAGAA AGGGCTCATT 1953
175
176 AAGCCTTTTG GACACAGGAC CCCAGAGAGG AAAAAGTGAC TTGCCCAAGG TCGTAAGCAA 2013
177
178 GCTACTGGCA TGGCAAGAGC CCAGCTTCCT GACGGAGCGC AACATTTCTC CACTGCACTG 2073
179
180 TGCTAGCAGC TCAGCAGGGC CTCTAACCTG TGATGTCACA CTCAAGAGGC CTTGGCAGCT 2133
181
182 CCTAGCCATA GAGCTTCCTT TCCAGAACCC TTCCACTGCC CAATGTGGAG ACAGGGGTTA 2193
183
184 GTGGGGCTTT CTATGGAGCC ATCTGCTTTG GGGACCTAGA CCTCAGGTGG TCTCTTGGTG 2253
185
186 TTAGTGATGC TGGAGAAGAG AATATTACTG GTTTCTACTT TTCTATAAAG GCATTTCTCT 2313
187
188 ATAAAAAAAA AAAAAA 2329
189
190

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 263 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

203 Met Leu Leu Ala Trp Val Gln Ala Phe Leu Val Ser Asn Met Leu Leu
204 -21 -20 -15 -10
205

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206 Ala Glu Ala Tyr Gly Ser Gly Gly Cys Phe Trp Asp Asn Gly His Leu
207 -5 1 5 10
208
209 Tyr Arg Glu Asp Gln Thr Ser Pro Ala Pro Gly Leu Arg Cys Leu Asn
210 15 20 25
211
212 Trp Leu Asp Ala Gln Ser Gly Leu Ala Ser Ala Pro Val Ser Gly Ala
213 30 35 40
214
215 Gly Asn His Ser Tyr Cys Arg Asn Pro Asp Glu Asp Pro Arg Gly Pro
216 45 50 55
217
218 Trp Cys Tyr Val Ser Gly Glu Ala Gly Val Pro Glu Lys Arg Pro Cys
219 60 65 70 75
220
221 Glu Asp Leu Arg Cys Pro Glu Thr Thr Ser Gln Ala Leu Pro Ala Phe
222 80 85 90
223
224 Thr Thr Glu Ile Gln Glu Ala Ser Glu Gly Pro Gly Ala Asp Glu Val
225 95 100 105
226
227 Gln Val Phe Ala Pro Ala Asn Ala Leu Pro Ala Arg Ser Glu Ala Ala
228 110 115 120
229
230 Ala Val Gln Pro Val Ile Gly Ile Ser Gln Arg Val Arg Met Asn Ser
231 125 130 135
232
233 Lys Glu Lys Lys Asp Leu Gly Thr Leu Gly Tyr Val Leu Gly Ile Thr
234 140 145 150 155
235
236 Met Met Val Ile Ile Ile Ala Ile Gly Ala Gly Ile Ile Leu Gly Tyr
237 160 165 170
238
239 Ser Tyr Lys Arg Gly Lys Asp Leu Lys Glu Gln His Asp Gln Lys Val
240 175 180 185
241
242 Cys Glu Arg Glu Met Gln Arg Ile Thr Leu Pro Leu Ser Ala Phe Thr
243 190 195 200
244
245 Asn Pro Thr Cys Glu Ile Val Asp Glu Lys Thr Val Val Val His Thr
246 205 210 215
247
248 Ser Gln Thr Pro Val Asp Pro Gln Glu Gly Ser Thr Pro Leu Met Gly
249 220 225 230 235
250
251 Gln Ala Gly Thr Pro Gly Ala
252 240
253

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 372 amino acids

(B) TYPE: amino acid

PAGE: 1

SEQUENCE VERIFICATION REPORT
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Original Text